

Y.Pak

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/618,623

DATE: 11/27/2001

TIME: 14:02:09

Input Set : A:\15060004.app

Output Set: N:\CRF3\11212001\I618623.raw

ENTERED

3 <110> APPLICANT: GROSS, RICHARD W.
4 MANCUSO, DAVID J.
6 <120> TITLE OF INVENTION: CALCIUM INDEPENDENT PHOSPHOILPASE A2Y POLYNUCLEOTIDES
7 AND POLYPEPTIDES AND METHODS THEREFOR
9 <130> FILE REFERENCE: 15060-0004
11 <140> CURRENT APPLICATION NUMBER: 09/618,623
12 <141> CURRENT FILING DATE: 2000-07-18
14 <160> NUMBER OF SEQ ID NOS: 47
16 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 782
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
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28 Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
29 20 25 30
31 Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg
32 35 40 45
34 Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
35 50 55 60
37 His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His
38 65 70 75 80
40 Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys
41 85 90 95
43 Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser
44 100 105 110
46 Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln
47 115 120 125
49 Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp
50 130 135 140
52 Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr
53 145 150 155 160
55 Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His
56 165 170 175
58 Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr
59 180 185 190
61 Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser
62 195 200 205
64 Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln
65 210 215 220
67 Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys
68 225 230 235 240
70 Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr
71 245 250 255
73 Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro

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74          260          265          270
76 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala
77          275          280          285
79 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly
80          290          295          300
82 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln
83 305          310          315          320
85 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys
86          325          330          335
88 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys
89          340          345          350
91 Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln
92          355          360          365
94 Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu
95          370          375          380
97 Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala
98 385          390          395          400
100 Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys
101          405          410          415
103 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly
104          420          425          430
106 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp
107          435          440          445
109 Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu
110          450          455          460
112 Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys
113 465          470          475          480
115 Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His
116          485          490          495
118 Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp
119          500          505          510
121 Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser
122          515          520          525
124 His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg
125          530          535          540
127 Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro
128 545          550          555          560
130 Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys
131          565          570          575
133 Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His
134          580          585          590
136 Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser
137          595          600          605
139 Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu
140          610          615          620
142 His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met
143 625          630          635          640
145 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val
146          645          650          655

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148 Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr
149          660          665          670
151 Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr
152          675          680          685
154 Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp
155          690          695          700
157 Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp
158 705          710          715          720
160 Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys
161          725          730          735
163 Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu
164          740          745          750
166 Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu
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180 <222> LOCATION: (1)..(2349)
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184 Met Ser Ile Asn Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn
185 1 5 10 15
187 gca aga agt gtt tgt ggg aag cag aga agc aag caa ctg tat ttc ttg 96
188 Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
189 20 25 30
191 ttc tca cct aag cat tac tgg agg ata agc cac atc agt cta caa aga 144
192 Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg
193 35 40 45
195 ggt ttt cat aca aac ata ata aga tgt aaa tgg acc aaa agt gaa gca 192
196 Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
197 50 55 60
199 cat tct tgc agt aag cac tgt tac tct cca agc aac cat ggt tta cat 240
200 His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His
201 65 70 75 80
203 att ggg att ttg aaa ctt agc act tct gct ccc aag gga ctt aca aaa 288
204 Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys
205 85 90 95
207 gtg aac att tgt atg tcc cgt att aaa agt act ttg aac tct gtt tca 336
208 Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser
209 100 105 110
211 aag gct gtt ttt ggc aat caa aat gaa atg att tca cgt tta gct caa 384
212 Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln
213 115 120 125
215 ttt aag cca agt tcc caa att tta aga aaa gta tcg gat agt ggc tgg 432

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216	Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg	Lys	Val	Ser	Asp	Ser	Gly	Trp	
217		130					135					140					
219	tta	aaa	cag	aaa	aac	atc	aaa	caa	gcc	atc	aaa	tct	ctg	aaa	aaa	tat	480
220	Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala	Ile	Lys	Ser	Leu	Lys	Lys	Tyr	
221	145					150					155					160	
223	agt	gac	aaa	tca	gca	gaa	aag	agt	cct	ttt	cca	gaa	gag	aaa	agt	cac	528
224	Ser	Asp	Lys	Ser	Ala	Glu	Lys	Ser	Pro	Phe	Pro	Glu	Glu	Lys	Ser	His	
225					165					170					175		
227	att	ata	gac	aaa	gaa	gaa	gat	ata	ggg	aaa	cgc	agt	ctt	ttt	cat	tac	576
228	Ile	Ile	Asp	Lys	Glu	Glu	Asp	Ile	Gly	Lys	Arg	Ser	Leu	Phe	His	Tyr	
229				180					185					190			
231	aca	agt	tct	ata	acc	aca	aaa	ttt	gga	gac	tca	ttc	tac	ttt	tta	tca	624
232	Thr	Ser	Ser	Ile	Thr	Thr	Lys	Phe	Gly	Asp	Ser	Phe	Tyr	Phe	Leu	Ser	
233			195					200					205				
235	aat	cat	att	aat	tca	tat	ttc	aaa	cgt	aag	gaa	aaa	atg	tct	caa	caa	672
236	Asn	His	Ile	Asn	Ser	Tyr	Phe	Lys	Arg	Lys	Glu	Lys	Met	Ser	Gln	Gln	
237		210					215					220					
239	aag	gaa	aat	gaa	cat	ttc	cgg	gac	aaa	tca	gaa	ctt	gaa	gat	aaa	aag	720
240	Lys	Glu	Asn	Glu	His	Phe	Arg	Asp	Lys	Ser	Glu	Leu	Glu	Asp	Lys	Lys	
241	225					230					235				240		
243	gta	gaa	gag	ggg	aaa	tta	aga	tct	cca	gat	cct	ggc	atc	ctg	gct	tat	768
244	Val	Glu	Glu	Gly	Lys	Leu	Arg	Ser	Pro	Asp	Pro	Gly	Ile	Leu	Ala	Tyr	
245				245					250					255			
247	aag	cca	ggc	tca	gaa	tct	gta	cat	acg	gtg	gac	aag	cct	aca	agt	cct	816
248	Lys	Pro	Gly	Ser	Glu	Ser	Val	His	Thr	Val	Asp	Lys	Pro	Thr	Ser	Pro	
249			260						265					270			
251	tct	gcg	ata	cct	gat	gtt	ctt	caa	gtt	tca	act	aaa	caa	agt	att	gct	864
252	Ser	Ala	Ile	Pro	Asp	Val	Leu	Gln	Val	Ser	Thr	Lys	Gln	Ser	Ile	Ala	
253			275				280					285					
255	aac	ttt	ctt	tct	cgt	ccc	acg	gaa	ggg	gta	caa	gct	tta	gta	ggg	ggg	912
256	Asn	Phe	Leu	Ser	Arg	Pro	Thr	Glu	Gly	Val	Gln	Ala	Leu	Val	Gly	Gly	
257		290					295				300						
259	tat	att	ggg	gga	ctt	gtc	ccc	aaa	tta	aag	tat	gat	tca	aag	agt	cag	960
260	Tyr	Ile	Gly	Gly	Leu	Val	Pro	Lys	Leu	Lys	Tyr	Asp	Ser	Lys	Ser	Gln	
261	305					310					315				320		
263	tca	gaa	gaa	cag	gaa	gag	cct	gct	aaa	act	gat	cag	gct	gtc	agc	aaa	1008
264	Ser	Glu	Glu	Gln	Glu	Glu	Pro	Ala	Lys	Thr	Asp	Gln	Ala	Val	Ser	Lys	
265				325						330				335			
267	gac	aga	aat	gca	gag	gag	aaa	aag	cgt	tta	tct	ctt	cag	cga	gaa	aag	1056
268	Asp	Arg	Asn	Ala	Glu	Glu	Lys	Lys	Arg	Leu	Ser	Leu	Gln	Arg	Glu	Lys	
269			340						345				350				
271	att	atc	gca	agg	gtg	agt	att	gat	aac	agg	acc	cgg	gca	tta	gtt	cag	1104
272	Ile	Ile	Ala	Arg	Val	Ser	Ile	Asp	Asn	Arg	Thr	Arg	Ala	Leu	Val	Gln	
273			355					360				365					
275	gca	tta	aga	aga	aca	act	gac	cca	aag	ctc	tgc	att	act	agg	gtt	gaa	1152
276	Ala	Leu	Arg	Arg	Thr	Thr	Asp	Pro	Lys	Leu	Cys	Ile	Thr	Arg	Val	Glu	
277		370					375					380					
279	gaa	ctg	act	ttt	cat	ctt	cta	gaa	ttt	cct	gaa	gga	aaa	gga	gtg	gct	1200
280	Glu	Leu	Thr	Phe	His	Leu	Leu	Glu	Phe	Pro	Glu	Gly	Lys	Gly	Val	Ala	

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285					405				410				415				
287	gat	gaa	act	ctt	cag	gct	gca	ggt	aga	gaa	att	ttg	gcc	cta	att	ggc	1296
288	Asp	Glu	Thr	Leu	Gln	Ala	Ala	Val	Arg	Glu	Ile	Leu	Ala	Leu	Ile	Gly	
289				420					425				430				
291	tat	gtg	gat	cca	gtg	aaa	ggg	aga	gga	atc	cga	att	ctc	tca	att	gat	1344
292	Tyr	Val	Asp	Pro	Val	Lys	Gly	Arg	Gly	Ile	Arg	Ile	Leu	Ser	Ile	Asp	
293				435					440				445				
295	ggt	gga	gga	aca	agg	ggc	gtg	ggt	gct	ctc	cag	acc	cta	cga	aaa	tta	1392
296	Gly	Gly	Gly	Thr	Arg	Gly	Val	Val	Ala	Leu	Gln	Thr	Leu	Arg	Lys	Leu	
297		450					455					460					
299	ggt	gaa	ctt	act	cag	aag	cca	ggt	cat	cag	ctc	ttt	gat	tac	att	tgt	1440
300	Val	Glu	Leu	Thr	Gln	Lys	Pro	Val	His	Gln	Leu	Phe	Asp	Tyr	Ile	Cys	
301	465				470					475						480	
303	ggt	gta	agc	aca	ggt	gcc	ata	tta	gct	ttc	atg	ttg	ggg	ttg	ttt	cat	1488
304	Gly	Val	Ser	Thr	Gly	Ala	Ile	Leu	Ala	Phe	Met	Leu	Gly	Leu	Phe	His	
305				485					490						495		
307	atg	ccc	ttg	gat	gaa	tgt	gag	gaa	ctt	tat	cga	aaa	tta	gga	tca	gat	1536
308	Met	Pro	Leu	Asp	Glu	Cys	Glu	Glu	Leu	Tyr	Arg	Lys	Leu	Gly	Ser	Asp	
309				500					505					510			
311	gta	ttt	tca	caa	aat	gtc	att	ggt	gga	aca	gta	aaa	atg	agt	tgg	agc	1584
312	Val	Phe	Ser	Gln	Asn	Val	Ile	Val	Gly	Thr	Val	Lys	Met	Ser	Trp	Ser	
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316	His	Ala	Phe	Tyr	Asp	Ser	Gln	Thr	Trp	Glu	Asn	Ile	Leu	Lys	Asp	Arg	
317		530					535					540					
319	atg	gga	tct	gca	ctg	atg	att	gaa	aca	gca	aga	aac	ccc	aca	tgt	cct	1680
320	Met	Gly	Ser	Ala	Leu	Met	Ile	Glu	Thr	Ala	Arg	Asn	Pro	Thr	Cys	Pro	
321	545				550						555				560		
323	aag	gta	gct	gct	gta	agt	acc	ata	gta	aat	aga	ggg	ata	aca	ccc	aaa	1728
324	Lys	Val	Ala	Ala	Val	Ser	Thr	Ile	Val	Asn	Arg	Gly	Ile	Thr	Pro	Lys	
325				565					570				575				
327	gct	ttt	gtg	ttc	aga	aac	tat	ggt	cat	ttt	cct	gga	atc	aac	tct	cat	1776
328	Ala	Phe	Val	Phe	Arg	Asn	Tyr	Gly	His	Phe	Pro	Gly	Ile	Asn	Ser	His	
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332	Tyr	Leu	Gly	Gly	Cys	Gln	Tyr	Lys	Met	Trp	Gln	Ala	Ile	Arg	Ala	Ser	
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335	tct	gct	gct	cca	ggc	tac	ttt	gca	gaa	tat	gca	ttg	gga	aat	gat	ctt	1872
336	Ser	Ala	Ala	Pro	Gly	Tyr	Phe	Ala	Glu	Tyr	Ala	Leu	Gly	Asn	Asp	Leu	
337		610					615					620					
339	cat	caa	gat	gga	ggt	ttg	ctt	ctg	aat	aac	cct	tcg	gca	tta	gct	atg	1920
340	His	Gln	Asp	Gly	Gly	Leu	Leu	Leu	Asn	Asn	Pro	Ser	Ala	Leu	Ala	Met	
341	625				630						635				640		
343	cat	gag	tgt	aaa	tgt	ctt	tgg	cca	gat	gtg	ccg	tta	gag	tgc	ata	gta	1968
344	His	Glu	Cys	Lys	Cys	Leu	Trp	Pro	Asp	Val	Pro	Leu	Glu	Cys	Ile	Val	
345				645					650						655		

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Output Set: **N:\CRF3\11212001\I618623.raw**

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L:2054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36